

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 18:23:55 ; Search time 2186.19 Seconds
(without alignments)
16364.623 Million cell updates/sec

Title: US-10-026-106E-9

Perfect score: 1772
Sequence: 1 aagggccatgscggggccgca.....acatccaccgagatcgatg 1472

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1:	em_estda:*
2:	em_esthm:*
3:	em_estin:*
4:	em_estnu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_hnc:*
9:	gb_estc:*
10:	gb_estc2:*
11:	gb_hnc:*
12:	gb_estc3:*
13:	gb_estc4:*
14:	gb_estc5:*
15:	em_estfun:*
16:	em_estom:*
17:	em_gse_hum:*
18:	em_gse_inv:*
19:	em_gse_pln:*
20:	em_gse_vrt:*
21:	em_gse_fun:*
22:	em_gse_mam:*
23:	em_gse_mus:*
24:	em_gse_pro:*
25:	em_gse_rod:*
26:	em_gse_phg:*
27:	em_gse_vrt1:*
28:	gb_gse1:*
29:	gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	598.8	40.7	1078	12	B0061188
2	477.6	32.4	508	10	BR244935
3	375.4	25.5	430	10	BR246345
4	372	25.3	836	13	BUI51377

C	5	370.4	25.2	991	12	B0056204
C	6	355.6	24.2	476	28	AQ610898
C	7	350.2	23.8	358	13	B0430530
C	8	348.4	23.7	964	13	BQ894374
C	9	341	23.2	640	14	BY729118
C	10	335	22.8	541	28	AQ610868
C	11	292	19.8	558	28	AQ634533
C	12	237.4	16.1	620	12	BT104593
C	13	237.8	15.2	496	14	CB713061
C	14	193.8	13.2	609	14	CB713061
C	15	188.2	12.8	606	28	BI657868
C	16	134.8	9.2	460	14	AQ772013
C	17	134.4	9.1	555	14	CB738101
C	18	89	6.0	392	13	BY093564
C	19	56.6	3.8	800	13	B0237675
C	20	55.2	3.8	663	12	BT043372
C	21	50.2	3.4	925	29	CNS0091P
C	22	47.4	3.2	391	14	CB775730
C	23	47.2	3.2	1201	13	BX381961
C	24	46.2	3.1	704	10	BG747302
C	25	44.8	3.0	485	13	BQ374676
C	26	43.8	3.0	341	29	B2367545
C	27	43.4	2.9	280	12	BI063605
C	28	43	2.9	709	28	B2121065
C	29	43	2.9	914	9	AL524362
C	30	42.4	2.9	967	12	BT108915
C	31	42.4	2.9	1020	13	BQ073607
C	32	42	2.9	878	13	B0911485
C	33	41.8	2.8	499	12	BJ059876
C	34	41.6	2.8	680	9	AV834441
C	35	41.6	2.8	931	29	CNS06SAL
C	36	41.4	2.8	682	28	AZ793096
C	37	41.2	2.8	334	13	BY103116
C	38	41.2	2.8	406	9	AV392658
C	39	41.2	2.8	450	9	AV392658
C	40	41.2	2.8	488	9	AV635124
C	41	41.2	2.8	504	9	AV388620
C	42	41.2	2.8	509	9	AV636333
C	43	41.2	2.8	519	9	AV390975
C	44	41.2	2.8	524	9	AV620459
C	45	41.2	2.8	550	9	AV392161

ALIGNMENTS

RESULT 1
B0061188
LOCUS
DEFINITION
AGENCOURT 6863006 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920208
5', mRNA Sequence.
ACCESSION
B0061188
VERSION
B0061188.1 GI:19864962
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1078)
NIH-MGC <http://mgc.ncl.nih.gov/>
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITL
JOURNAL
COMMENT
Contact: Robert Strussberg, Ph.D.
Email: cgapdb-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMU at:
<http://image.llnl.gov>
Plate: LLCM2083 row: 1 column: 09
High quality sequence stop: 593.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5920208"
/issue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/note="Organ: lymph; Vector: pOT87; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 243 a 306 c 309 g 219 t 1 others

Query Match 40.7%; Score 598.8; DB 12; Length 1078;
Best Local Similarity 96.1%; Pred. No. 4.6e-126;
Matches 624; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

16 CCCGAGCGCTGGGCGCCCTGCTCTGCTGCTGCAAGCCCTCCAG--GGAGGCCCC 73
108 CCCGAGCAAGCAAGCACTGAGGCTCTGGGCGCTGCGCTCCCGGAGAGAGAGGCCCC 167
74 GTCTGAGCCCTCCCAAGATGTAGACCTCTCTCCCAAGATTCAGCGTACCTGACAT 133
168 GTCTGAGCCCTCCCAAGATGTAGACCTCTCTCCCAAGATTCAGCGTACCTGACAT 227
134 GGCTCCAGGCGCTGGAGAACCCCAAGATGTAGACCTATTTGTGGCTATCAGAGTCTC 193
228 GGCTCCAGGCGCTGGAGAACCCCAAGATGTAGACCTATTTGTGGCTATCAGAGTCTC 287
194 CCACCGGTAGACGGTGGCGGAGGTGAAGATGTGGCGGAGCCAGAGAGCTCTATGTT 253
288 CCACCGGTAGACGGTGGCGGAGGTGAAGATGTGGCGGAGCCAGAGAGCTCTATGTT 347
254 CATGATGTGCTGAAGAAACAGAGCTGTACAAAGATTGAAGAGAGGCGGTGGAGCG 313
348 CATGATGTGCTGAAGAAACAGAGCTGTACAAAGATTGAAGAGAGGCGGTGGAGCG 407
314 TTCTCCAGCTCAAGTCCCTGGAGTGAAGTCCGAATACCTGATTAATCTTTTGAAG 373
408 TTCTCCAGCTCAAGTCCCTGGAGTGAAGTCCGAATACCTGATTAATCTTTTGAAG 467
374 TGGAGCGGCGGCGGAGCTGTCTGATGTACCAAGAGAGAGATCTGAGTGGCAATG 433
468 TGGAGCGGCGGCGGAGCTGTCTGATGTACCAAGAGAGATCTGAGTGGCAATG 527
434 CCAGGTACCAAGTCCCTGGAGTGAAGTCCGAATACCTGATTAATCTTTTGAAG 493
528 CCAGGTACCAAGTCCCTGGAGTGAAGTCCGAATACCTGATTAATCTTTTGAAG 587
494 GGAAGAGAGGCGGAGAAACAGACCTATTTTCAGTCACTCCCATGAGCGAGAGTCC 553
588 GGAAGAGAGGCGGAGAAACAGACCTATTTTCAGTCACTCCCATGAGCGAGAGTCC 647
554 AATATCACTCTCAAGCAAGCTGCCAGAGAAACCACTGCTCAGTGGCGAAGCAATCTACA 613
648 AATATCACTCTCAAGCAAGCTGCCAGAGAAACCACTGCTCAGTGGCGAAGCAATCTACA 707
614 CGTTAGTGTCCGAAAATACAGCAAGTCTCTTAAGCCCACTGCTTCTT 662
708 CGTTAGTGTCCGAAAATACAGCAAGTCTCTTAAGCCCACTGCTTCTT 756

RESULT 2
BE244935 508 bp mRNA linear EST 03-OCT-2001
LOCUS

DEFINITION
TCBAP2669 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP2669, mRNA
sequence.
ACCESSION
BR244935
VERSION
BR244935.1 GI:9096765
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 508)
Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.,
Bouck, J., Gbabe, R.A. and Margolin, J.F.
Pediatric Leukemia cDNA Sequencing Project
Unpublished
TITLE
JOURNAL
COMMENT
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MCJ-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@ccc.org
Citation: Carninci, P. and Hayashizaki, Y. High efficiency
full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Seq primer: M13 primer

FEATURES
Location/Qualifiers
1. 508
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCBAP2669"
/sex="male"
/tissue_type="leukophereasts"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia Baylor-HGSC project-TCBA"
/note="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer (5'GGAGAGCTCAGCGCGCGGAGAGAGCT)VN
3'; 5'-A.C.G./N.A.C.G./T and then dg tailed. Second strand
was primed with a BamHI-dC primer
(5'AGAGAGCTCGATCCGCGCGCGGAGAGAGATTAAT(C)3').
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda pSB vector. Library was constructed by Wei Yu at RIKEN
of Japan (Carninci P., Westover A., Nishiyama Y., Ohsumi T.,
Itoh M., Nagaoka S., Sasaki, N., Okazaki Y., Muramatsu M.,
Schneider C., Hayashizaki Y. High efficiency selection of
full-length cDNA by improved biotinylated cap trapper.,
DNA Res 4: 1, 61-6, Feb 28, 1997)".

BASE COUNT 108 a 147 c 160 g 93 t

Query Match 32.4%; Score 477.6; DB 10; Length 508;
Best Local Similarity 98.4%; Pred. No. 1.6e-98;
Matches 504; Conservative 4; Mismatches 4; Indels 4; Gaps 2;

798 TCGAGGCGCCGAGCAAGCAAGATGTGAAGAGAGCTTGACAGAGCAAGAGAG 857
1 TCGAGGCGCCGAGCAAGCAAGATGTGAAGAGAGCTTGACAGAGCAAGAGAG 60
858 AGAGATGTGAAGAGCAAGAGATGTGAGCTTCCAGCTTCACTTGAACCACTT 917
61 AGAGATGTGAAGAGCAAGAGATGTGAGCTTCCAGCTTCACTTGAACCACTT 119
918 CTTTCCGAGGAGCAAGAGCAAGAGCTTCCAGGAGCTTCCAGGAGCTTCCAGG 977
120 CTTTCCGAGGAGCAAGAGCAAGAGCTTCCAGGAGCTTCCAGGAGCTTCCAGG 116
978 CAGGAGGCGCCGAGGAGCTCTGAGTCCCAAGCAAGAGCTCTGCTTGGAGATTCTTCA 1037

High quality sequence stop: 522.
Location/Qualifiers

FEATURES
source
1. 836
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6104649"
/issue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 185 a 223 c 240 g 186 t 2 others

ORIGIN

Query Match 25.3%; Score 372; DB 13; Length 836;
Best Local Similarity 99.2%; Pred. No. 2.4e-74;
Matches 385; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

674 CAGGACTTTTCTGACACACACACCTTGTGGCACTTTCAGCCGACGACGACGATCC 733
541 CAGGACTTTTCTGACACACACACCTTGTGGCACTTTCAGCCGACGACGATCC 482
734 GTGAATGACTTGTCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 793
481 GTGAATGACTTGTCT 422
794 CAGGACTTTTCTGACACACACACCTTGTGGCACTTTCAGCCGACGACGATCC 853
421 CAGGACTTTTCTGACACACACACCTTGTGGCACTTTCAGCCGACGACGATCC 362
854 GAGGAGGAGATGAGAGGACACAGAGATGGCTCAGCTTCCAGCCCTTACATTGAACA 913
361 GAGGAGGAGATGAGAGGACACAGAGATGGCTCAGCTTCCAGCCCTTACATTGAACA 302
914 CTTCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 973
301 CTTCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 245
974 GACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1033
244 GACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 185
1034 TCAGACAGAGAGCTGGGCGCAGCACTGTGG 1061
184 TCAGACAGAGAGCTGGGCGCAGCACTGTGG 157

RESULT 5
B0056204/c 991 bp mRNA linear EST 29-MAR-2002
LOCUS AGENCOURT 6773374 NIH_MGC_99 Homo sapiens CDNA clone IMAGE:5808505
DEFINITION 5' mRNA sequence.

ACCESSION B0056204
VERSION B0056204.1 GI:19815544
KEYWORDS EST

ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
KEYWORDS Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 991)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Straube, Ph.D.
Email: cgaaba-remail.nih.gov

Tissue Procurement: Lou Straube
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM2052 row: k column: 02
High quality sequence stop: 645.
Location/Qualifiers

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5808505"
/issue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 224 a 285 c 270 g 211 t 1 others

ORIGIN

Query Match 25.2%; Score 370.4; DB 12; Length 991;
Best Local Similarity 99.0%; Pred. No. 6e-74;
Matches 384; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

674 CAGGACTTTTCTGACACACACCTTGTGGCACTTTCAGCCGACGACGATCC 733
541 CAGGACTTTTCTGACACACACCTTGTGGCACTTTCAGCCGACGACGATCC 482
734 GTGAATGACTTGTCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 793
481 GTGAATGACTTGTCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 422
794 CAGGACTTTTCTGACACACACCTTGTGGCACTTTCAGCCGACGACGATCC 853
421 CAGGACTTTTCTGACACACACCTTGTGGCACTTTCAGCCGACGACGATCC 362
854 GAGGAGGAGATGAGAGGACACAGAGATGGCTCAGCTTCCAGCCCTTACATTGAACA 913
361 GAGGAGGAGATGAGAGGACACAGAGATGGCTCAGCTTCCAGCCCTTACATTGAACA 302
914 CTTCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 973
301 CTTCTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 245
974 GACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1033
244 GACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 185
1034 TCAGACAGAGAGCTGGGCGCAGCACTGTGG 1061
184 TCAGACAGAGAGCTGGGCGCAGCACTGTGG 157

RESULT 6
A0610898/c 476 bp DNA linear GSS 15-JUN-1999
LOCUS AG610898
DEFINITION HS 5105 A2 G06 SP6E RPCT-11 Human Male BAC Library Homo sapiens
genomic clone Plate=681 Col=12 Row=M, genomic survey sequence.

ACCESSION A0610898
VERSION A0610898.1 GI:5072174
KEYWORDS GSS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens

Oy 245 TGGATGTTCTATGATGCTGAGGAAAGAGACCTGTAACAGAGTTCAAGGAGCGG 304
 Db 243 TGGATGTTCTATGATGCTGAGGAAAGAGACCTGTAACAGAGTTCAAGGAGCGG 302
 Oy 305 TGGGACGGTTTCTCCAGCTCCAGAGTCCCTGGGTGAGATCCGAATACCTGGAT 360
 Db 303 TGGGACGGTTTCTCCAGCTCCAGAGTCCCTGGGTGAGATCCGAATACCTGGAT 358
 RESULT 8
 B0894374 964 bp mRNA linear EST 16-AUG-2002
 LOCUS B0894374
 DEFINITION AGENCOURT_8623992 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6304287
 5', mRNA sequence.
 VERSION B0894374
 KEYWORDS B0894374.1 GI:22286388
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 964)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/MLND at:
 http://image.llnl.gov
 Plate: L1CM2524 row: 1 column: 16
 High quality sequence scope: 510.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="6304287"
 /tissue_type="lymphoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
 BclRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GCGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."
 BASE COUNT 196 a 277 c 268 g 223 t
 ORIGIN
 Query Match 23.7% Score 348.4; DB 13; Length 964;
 Best Local Similarity 98.5%; Pred. No. 6,2e-69;
 Matches 384; Conservative 1; Indels 5; Gaps 3;

Oy 852 AAGAGAGAGATGATGAGAGACACAGAGATGAGCGCTTCCAGCCCTACATTGAC 911
 Db 377 AAGAGAGAGATGATGAGAGACACAGAGATGAGCGCTTCCAGCCCTACATTGAC 918
 Oy 912 CACCTTCTTCTCTGGGACCAAGACACAGAGCTCCAGGACCTCGAGAGCC??TGGTGGG 971
 Db 317 CACCTTCTTCTCTGGGACCAAGACACAGAGCTCCAGGACCTCGAGAGCC--TGGTGGG 261
 Oy 972 TGAAGTCAAGAGAGCCCAAGGAGCTCTGTGCTCCAAAGCAAGCTCTGTGAGGATT 1031
 Db 260 TGAAGTCAAGAGAGCCCAAGGAGCTCTGTGCTCCAAAGCAAGCTCTGTGAGGATT 201
 Oy 1032 CTTCAAGACAGAGCTGGGCGACACTGTGG 1061
 Db 200 CTTCAAGACAGAGCTGGGCGACACTGTGG 171
 RESULT 9
 B0729118 640 bp mRNA linear EST 17-DEC-2002
 LOCUS B0729118
 DEFINITION B0729118 RIKEN full-length enriched, 7 days embryo whole body Mus
 musculus cDNA clone C430033A03 5', mRNA sequence.
 VERSION B0729118
 KEYWORDS B0729118.1 GI:27142245
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 640)
 AUTHORS Okazaki, Y., Putnam, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Mikado, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,
 Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C.,
 Gojobori, T., Baldarelli, R., Hill, D. P., Bulc, C., Hume, D. A.,
 Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,
 Beisel, K. W., Blake, J. A., Brad, D., Bryant, C., Chochia, C., Corbett,
 L. E., Cousins, S., Dalle, E., Dragani, T. A., Fletcher, C. F., Forrest,
 A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Glast, C., Godzik, A.,
 Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, J. J.,
 Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedierski, R. M.,
 King, B. L., Kongaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons,
 P. A., Maglott, D. R., Maltara, L., Marchionni, L., McKenzie, L., Miki,
 H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G.,
 Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D.,
 Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring,
 B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou,
 M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale,
 R. D., Tomita, M., Verrado, R., Wagner, L., Wahlestedt, C., Wang, Y.,
 Watanabe, Y., Wells, C., Wilm, L. G., Wrynshaw-Borls, A., Yang, Y.,
 Yang, Y., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
 Carninci, P., Hayashizumi, N., Hirozane-Kashikawa, T., Kono, H., Nakamura,
 M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Waki, J., Aizawa, K.,
 Arikawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,
 Y., Itoh, M., Kikawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata,
 K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,
 E. S., Rogers, D., Birney, E. and Hayashizumi, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 TITLE JOURNAL MEDLINE
 PUBMED 22354683
 COMMENT Contact: Yoshihide Hayashizumi,
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenho-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda,
 S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K.,

Db 473 CTGTCCAAA--GAACTGCCAGAGGGGTCCAGCCCTCCAGTCAAGGCTCCGAC 416
 QY 811 CACCCACAGACAGATGAGAGAGACCTTGACAGAGAGAGAGAGAGATGAGAG 870
 Db 415 CACACACAGAGAGATGAGAGAGAGCTCTTGACAGAGAGAGAGAGATGAGAG 356
 QY 871 GAGACAG 930
 Db 355 GACACAG 296
 QY 931 AGAGACAG 990
 Db 295 AGAGACAG 239
 QY 991 GGCCTCTGTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
 Db 238 GGCCTCTGTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179
 QY 1051 CAGCAGCTGTGAGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1110
 Db 178 CAGCAGCTGTGAGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 119
 QY 1111 GCCAG 1156
 Db 118 AGCAG 73

RESULT 11
 A0634533 558 bp DNA linear GSS 17-JUN-1999
 LOCUS RPCI-11-478C4.TV RPCI-11 Homo sapiens genomic clone RPCI-11-478C4,
 DEFINITION genomic survey sequence.
 A0634533
 VERSION A0634533.1 GI:50971468
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
 J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished
 COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@jg.med.buffalo.edu). Clones may be purchased from
 BACRAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genet cs (info@regen.com). BAC end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: 17
 Class: BAC ends.

FEATURES

source
 Location/Qualifiers
 1..558
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="GDB:768319"
 /db_xref="taxon:9606"
 /clone="RPCI-11-478C4"
 /sex="Male"
 /cell_type="lymphocytes"
 /clone_id="RPCI-11"
 /note="Vector: pBac3.6; Site 1: EcoRI; Site 2: EcoRI;
 RPCI11 Human Male BAC Library"

BASE COUNT 113 a 156 c 180 g 109 t
 ORIGIN
 Query Match 19.8%, Score 292, DB 28; Length 558;
 Best Local Similarity 100.0%; Pred. No. 3.8e-56;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1181 GGTTCCTGGAAGAGCTCCAGAGATACCTCTCTCTGAGGCACTGAGGCACTTA 1240
 Db 1 GGTTCCTGGAAGAGCTCCAGAGATACCTCTCTCTGAGGCACTGAGGCACTTA 60
 QY 1241 CCACCCGAGCCGAACTGTGCTCCCTGAGGAGACCCGAGTTCTCTTCAGACACTGACCTTG 1300
 Db 61 CCACCCGAGCCGAACTGTGCTCCCTGAGGAGACCCGAGTTCTCTTCAGACACTGACCTTG 120
 QY 1301 TGTGTGGAAG 1360
 Db 121 TGTGTGGAAG 180
 QY 1361 GATCGGGAGAGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1420
 Db 181 GATCGGGAGAGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 QY 1421 GGGCATTACATGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1472
 Db 241 GGGCATTACATGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 292

RESULT 12
 B1104593 620 bp mRNA linear EST 26-JUN-2001
 LOCUS B1104593
 DEFINITION 602891434P1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGB:5036481 5',
 mRNA sequence.
 B1104593
 VERSION B1104593.1 GI:14555486
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Binkley,C., Metaxas,C., Choudhary, S., Vertebate, Buteleostomi,
 Mammalia; Butheria; Primates; Catarrhini; Homindae; Homo.
 TITLE (Bases 1 to 620)
 JOURNAL NIH-MGC http://mgi.nci.nih.gov/
 COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov
 plate: LLNL1101 row: c column: 10
 High quality sequence start: 5
 High quality sequence stop: 556
 Location/Qualifiers
 1..620

FEATURES

source
 Location/Qualifiers
 1..620
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGB:5036481"
 /tissue_type="spontaneous tumor, metastatic to mammary."
 /cell_type="mammary."
 /lab_host="DHL0B"
 /clone_id="NCI_CGAP_Lu29"
 /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.
 library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"
 BASE COUNT 140 a 186 c 168 g 126 t
 ORIGIN

Query Match 16.1%; Score 237.4; DB 12; Length 620;
 Best Local Similarity 71.5%; Pred. No. 1.1e-43; Indels 13; Gaps 6;
 Matches 398; Conservative 0; Mismatches 146;

7 ATGCGGAGGCGCGGAGCGCTGGGGCCCTGCTCTG-TGCTGCTGAG-GCCGCTCAG 64
 |||||
 16 ATGTGGGGGGCGGCGGCTGGGGCCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 75
 |||||
 65 GAGAGCGCGCGCTGGGGCCCTGCGGAGATGAGCGCTGCTGCGGAGCTTCAAGCGCT 124
 |||||
 76 GAGAGCGCGCGCTGAGCGCGCGGAGATGAGCGCTGCTGCGGAGCTTCAAGCGCT 135
 |||||
 125 ACTGACATGCTGCGGAGCGCTGCGGAGATGAGCGCTGCTGCGGAGCTTCAAGCGCT 184
 |||||
 136 ACTGACATGCTGCGGAGCGCTGCGGAGATGAGCGCTGCTGCGGAGCTTCAAGCGCT 195
 |||||
 185 AGAGCTCTCCAGCGCGGAGCGCTGCGGAGATGAGCGCTGCTGCGGAGCTTCAAGCGCT 244
 |||||
 196 AAGAGCTCTCCAGCGCGGAGCGCTGCGGAGATGAGCGCTGCTGCGGAGCTTCAAGCGCT 252
 |||||
 245 TGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
 |||||
 253 TGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
 |||||
 304 GTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 363
 |||||
 313 GTACAGGCGGCTTCCGCGAGGCGGAGCTTCCGCGAGGCTGCTGCTGCTGCTGCTGCTGCT 372
 |||||
 364 CTTTGTGAGTGAAGCG 423
 |||||
 373 CTTTGTGAGTGAAGCG 432
 |||||
 424 AGTCCAGTGAAGCG 483
 |||||
 433 AGGAGTGAAGCG 490
 |||||
 484 GTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
 |||||
 491 GTGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
 |||||
 539 ATGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 555
 |||||
 551 ATGCGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 567
 |||||

RESULT 13
 CB713061 496 bp mRNA linear EST 10-APR-2003
 LOCUS AMGNNUC:NRHY5-00223-G11-A W Rat hypothalamus (10471) Rattus
 DEFINITION norvegicus cDNA clone nrhy5-00223-g11 5', mRNA sequence.
 CB713061
 ACCESSION CB713061.1 GI:29770209
 VERSION EST.
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 496)
 AUTHORS Amgen EST Program.
 TITLE Amgen Rat EST Program
 JOURNAL Unpublished
 COMMENT Contact: Dan Fitzpatrick
 Amgen, Inc
 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00223 row: 9 column: 11.
 Location/Qualifiers
 1..496
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"

Query Match 15.2%; Score 223.8; DB 14; Length 496;
 Best Local Similarity 72.4%; Pred. No. 1.3e-40; Indels 29; Gaps 2;
 Matches 331; Conservative 0; Mismatches 97;

7 ATGCGGAGGCGCGGAGCGCTGGGGCCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 66
 |||||
 55 ATGTGGGGGGCGGCGGCTGGGGCCCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 114
 |||||
 67 AGGCGCGGCTGCGGCG 126
 |||||
 115 AGGCGCGGCTGCGGCG 174
 |||||
 127 CTGACATGCTGCGGAGCGCTGCGGAGATGAGCGCTGCTGCGGAGCTTCAAGCGCT 186
 |||||
 175 CTGACATGCTGCGGAGCGCTGCGGAGATGAGCGCTGCTGCGGAGCTTCAAGCGCT 234
 |||||
 187 AGCTCTCCAGCGCGGAGCGCTGCGGAGATGAGCGCTGCTGCGGAGCTTCAAGCGCT 246
 |||||
 235 AGCTCTCCAGCGCGGAGCGCTGCGGAGATGAGCGCTGCTGCGGAGCTTCAAGCGCT 288
 |||||
 247 CTATGCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 306
 |||||
 289 GTGTGTCTCCAGTGAAGTCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 348
 |||||
 307 CGGAGGCTTCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
 |||||
 349 GAGGAGCTTCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 390
 |||||
 367 TTTGAGATGAGAGCG 426
 |||||
 391 ----AGTGAAGCTGAGCG 445
 |||||
 427 GCCATGCGGAGTACGAGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 463
 |||||
 446 GTACAGGCTTCTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 482
 |||||

RESULT 14
 B1657668 609 bp mRNA linear EST 12-SEP-2001
 LOCUS B1657668 60381241P1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5325586 5',
 DEFINITION mRNA sequence.
 B1657668
 ACCESSION B1657668.1 GI:15571904
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 609)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cga@b6-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Princeton University
 Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMU at:
 http://image.llnl.gov
 Plate: L1AM1826 row: a column: 11
 High quality sequence stop: 609.

FEATURES
source

Location/Qualifiers
1. 609
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:532586"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Map4"
/note="Organ: mammary; Vector: pCMV-Sport6; Site 1: SalI; Site 2: NotI. Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Firth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."

BASE COUNT 145 a 176 c 162 g 126 t

ORIGIN

Query Match 13.2%; Score 193.8; DB 12; Length 609;
Best Local Similarity 71.0%; Pred. No. 1e-33;
Matches 284; Conservative 0; Mismatches 110; Indels 6; Gaps 2;

674 CAGACCTTCTGACACACACACCTTGGCACTTTCCGCCGACGACAGATCC 733
189 CAGACCTTCTGACACACACACCTTGGCACTTTCCGCCGACGACAGATCC 248
734 GTGATGACTTGTCTCTGTCCTCCGAAAGAACTGACGAGGGGTCAAGCCGCT 793
249 TCTGATGACTTGTCTCTGTCCTCCGAAAGAACTGACGAGGGGTCAAGCCGCT 308
794 CGAGTCAGGGGCCCCAGCCCAAGACAGAAAGAAAGAAAGAAAGAAAGAAAGAA 853
309 CAGGTCAAGAAACCCAGCCAGCTTACAGGAGACCAAGAAAGAAAGAAAGAAAG 368
854 GAGGAGAGAGATGAGAGACACAGAAAGTGGCTTCAAGCTTCAATTAACCA 913
369 GACGAGAGACACAGACTACGAA--TGACGACGGTACAGGCTTCAAGCTTCAAG 425
914 CCTTCTTCTGAGGAGACAGACAGGCTTCAAGGAGCTTCAAGGCTTCAAGGAG 970
426 CCCCCTTCTGAGGAGAGAGAGGCTTCAAGGAGCTTCAAGGAGCTTCAAGGAG 485
971 GTGACTCAGGAGAGGAGGCTTCTGCTGCTCAAGGAGGAGGAGGAGGAGGAG 1030
486 GTGATTCAGGAGGAGGCTTCTGCTGCTCAAGGAGGAGGAGGAGGAGGAGGAG 545
1031 TCTTCAGACAGAGCTGGGCGACAGCTGAGCTTCTCT 1070
546 TCTTCAGACAGAGCTGGGCGACAGCTGAGCTTCTCT 585

RESULT 15
A0772013c 506 bp DNA linear GSS 29-JUL-1999
LOCUS HS_5413_B2_H01_SPEB_RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION A0772013 genomic clone Place=989 Col=2 Row=P, genomic survey sequence.
ACCESSION A0772013
VERSION A0772013.1 GI:5651741
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 506)
Mamaitas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589

PUBMED
COMMENT 10449764
Contact: Mamaitas G.G., Wallace J.C., Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.hnrc.washington.edu
plate: 989 row: P column: 2
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 506.

FEATURES
source

Location/Qualifiers
1. 506
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=989 Col=2 Row=P"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBAC3.6 vector at EcoRI sites"

BASE COUNT 111 a 153 c 97 g 144 t 1 others

ORIGIN

Query Match 12.8%; Score 188.2; DB 28; Length 506;
Best Local Similarity 80.1%; Pred. No. 1.8e-32;
Matches 258; Conservative 0; Mismatches 59; Indels 5; Gaps 3;

839 CTTCAGAGACGAAAGAGAGAGATGAGAGAGACACAGAAATGGCTTCACTTCAG 898
322 CTTCAGATGACAAAGAGATGAGATG--GAGAGACACATGATGATTAAGTACCA 264
899 CCTTATATGAAACACCTTCTCTGAGGAGCAAGAGACAGGCTTCAAGGAGGAG 958
263 CCTTATATGAAACCTTCTCTGATGATGAGG--AAGAGCTTCAAGGCTTCAAGG 205
959 GCCTTCTGAGGAGTCAAGAGAGGAGGAGGCTTCTGCTTCAAGGAGGAGGCTCC 1018
204 TC--TGAGGAGGAGTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 148
1019 TCTGCTTGGATTTCTTCAAGAGAGTGGGCGACAGCTGAGACTCTCTGAGACAG 1078
147 TCTGCTTGGATTTCTTCAAGAGAGTGGGCGACAGAGTGGGAGCTCTCTGAGACAG 88
1079 GCTGGTCTCTGCTATTTGGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1138
87 GCTGGTCTCTGCTATTTGGCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 28
1139 CACCAAGATCTCTCCACAC 1160
27 CACCAAGATCTTACACTCCAC 6

Search completed: September 17, 2003, 22:13:27
Job time : 2189.19 secs